Appln. No. 10/515,493
Amendment dated January 19, 2010
Reply to Office Action of Aug. 31, 2009

Atty Dkt: RUSSELL-3

IN THE SPECIFICATION

At page 39, please amend the paragraph at lines 4-25, as follows:

Example 1 - Haplotype clade deduction
First haplotypes of the PAI-1 gene (Figure 1) were deduced, the major haplotype clades were
identified (Figures 1 and 2), and a minimum set of htSNPs defining the major haplotype clades
(Figure 1) were selected. The htSNPs and the 4G/5G polymorphism were in Hardy-Weinberg
equilibrium (Table 2). Furthermore, it was found that haplotypes containing the 4G allele could
be grouped into the allele that contained the minor T allele of a C/T polymorphism at position
13985 and the allele that contained the minor G allele of a T/G polymorphism at position 12580
(Figures 1 and 2). The haplotype map in Figure 1, shows PAI-1 gene haplotypes in Caucasians.
Haplotypes were inferred using PHASE from available data, and represented in the style of
PATIL et al. (*Science* (2001) *294*(5547):1669-70). Columns indicate polymorphic loci and rows
indicate distinct haplotypes inferred in Caucasian individuals. Light cells indicate rare alleles,
and dark cells indicate common alleles. The map was generated from genotype data (available
publicly at the URL on the Worldwide web [[http://]pga.mbt.washington.edu/ and at
SeattleSNPs NHLBI Program for Genomic Applications, SeattleSNPs, Seattle, WA) of 23
unrelated Caucasians from the Coriell registry of patients. Haplotypes were inferred using the
statistical program PHASE 2.0 (Stephens M and Donnelly P, *Am J Human Genet*. (2003)
73(6):1162-1169). Polymorphisms that provide the same information as the 12580G allele were
chosen based on this haplotype map. These polymorphisms provide the same information as the
12580G allele. One method is to positively identify the 12580G allele (section A) either directly
or in combination. Another method is to positively identify the 12580T allele (section B), either
directly or in combination, and thereby negatively identify the 12580G allele. Haplotypes within
each clade are very similar, while clades differ substantially from each other. MEGA II was used
to sort haplotypes into clades separated by heavier lines.